In the Specification:

Please amend the specification as shown:

Please delete paragraph [0118] and replace it with the following paragraph:

[0118] Cocoons from Bombyx Mori were boiled for 1 hour in an aqueous solution of 0.02M Na2CO3, and rinsed with water to extract sericins. Purified silk was solubilized in 9M LiBr solution and dialyzed (Pierce, MWCO 2000 g/mol) against PBS for 1 day and again against 0.1M MES, 0.5 M NaCl, pH 6 buffer for another day. An aliquot of the silk solution was coupled with GRGDS (SEQ ID NO: 7) peptide to obtain RGD-silk. For coupling COOH groups on the silk were activated by reaction with 1-ethyl-3-(dimethylaminopropyl)carbodiimide hydrochloride (EDC)/ N-hydroxysuccinimide (NHS) solution for 15 minutes at room temperature (Sofia et al. 2001. J Biomed Mater Res 54:139-148). To quench the EDC, 70 µl/ml β-mercaptoethanol was added. Then 0.5 g/l peptide was added and left for 2 hours at room temperature. The reaction was stopped with 10 mM hydroxylamine. Silk solutions were dialyzed against 0.1 M 2-(N-morpholino)-ethanesulfonic acid buffer, pH 4.5-5 for 1 day. Silk and Silk-RGD solutions were lyophilized and redissolved in hexafluoro-2-propanol (HFIP) to obtain a 17% (w/v) solution. Granular NaCl was weighed in a Teflon container and silk/HFIP solution was added at a ratio of 20:1 (NaCl/silk). HFIP was allowed to evaporate for 2 days and NaCl/silk blocks were immersed in 90% (v/v) methanol for 30 minutes to induce a protein conformational transition to β-sheet (Nazarov et al. 2003. In Department of Biomedical Engineering. Medford: Tufts University). Blocks were removed, dried and NaCl was extracted in water for 2 days. Disk shaped scaffolds (5 mm diameter, 2 mm thick) were prepared using a dermal punch (Miltey, Lake Success, NY), and autoclaved.

Please delete paragraph [0142] and replace it with the following paragraph:

[0142] Cocoons from Bombyx Mori (Linne, 1758) were boiled for 1 hour in an aqueous solution of 0.02M Na2CO3, and rinsed with water to extract sericins. Purified silk was solubilized in 9M LiBr solution and dialyzed (Pierce, Woburn, MA; MWCO 3500 g/mol) against water for 1 day and again against 0.1M MES (Pierce), 0.5 M NaCl, pH 6 buffer for another day. An aliquot of the silk solution was coupled with glycine-arginine-alanineglycine-aspartate-serine (GRGDS; SEQ ID NO: 7) peptide to obtain RGD-silk. For coupling COOH groups on the silk were activated by reaction with 1-ethyl-3-

(dimethylaminopropyl)carbodiimide hydrochloride (EDC)/ N-hydroxysuccinimide (NHS) solution for 15 minutes at room temperature (Sofia et al. 2001. J Biomed Mater Res 54:139-148). To quench the EDC, 70 µl/ml β-mercaptoethanol was added. Then 0.5 g/l peptide was added and left for 2 hours at room temperature. The reaction was stopped with 10 mM hydroxylamine. Silk solutions were dialyzed against water for 2 days. Silk and Silk-RGD solutions were lyophilized and redissolved in hexafluoro-2-propanol (HFIP) to obtain a 17% (w/v) solution. Granular NaCl was weighed in a Teflon container and silk/HFIP solution was added at a ratio of 20:1 (NaCl/silk). HFIP was allowed to evaporate for 2 days and NaCl/silk blocks were immersed in 90% (v/v) methanol for 30 minutes to induce a protein conformational transition to β-sheets (Nazarov et al. 2003. In Department of Biomedical Engineering. Medford: Tufts University). Blocks were removed, dried and NaCl was extracted out in water for 2 days. Disk shaped scaffolds (5 mm diameter, 2 mm thick) were prepared using a dermal punch (Miltey, Lake Success, NY), and autoclaved.

Please delete paragraph [0144] and heading and replace it with the following paragraph and heading:

Iodiniation of GRYDS (SEQ ID NO: 8) peptide

[0144] To assess the amount of bound RGD to the scaffolds, GRYDS (SEQ ID NO: 8) -peptide was iodinated with non radioactive iodine to quantify the amount of bound peptide in the silk film surface by X-ray photoelectron spectrometer (XPS). The procedure involved first flusing of Sep-Pak C18 reverse phase cartridge (Waters) with 10 ml of a 80:20 mix of methanol:water and then flushing with 10 ml of 0.1M PBS 0.5 NaCl pH=6 buffer, as previously described (Sofia et al. 2001. J Biomed Mater Res 54:139-148). Three IODO-BEADS (Pierce) were rinsed once with 1 ml of PBS buffer. Eighty ml of PBS and then 10 µl of 3.75 g/L NaI in PBS were added and the activation was allowed for 5 minutes. Then, 1 ml of 0.1 g/l GRYDS (SEQ ID NO: 8) peptide in PBS was added and the reaction was allowed for 15 min. Beads were rinsed with PBS and the peptide solution was injected into the C18 column followed by elution with 0, 20, 40, and 60% methanol in water solutions. Fractions were collected and analyzed at 280 nm. The iodination procedure was repeated with the same peptide through lyophilization of the desired fractions and resolubilizing in buffer to achieve the desired extent of iodination (1 atom of iodine per molecule of GRYDS; SEQ ID NO: 8). Iodinated peptide was coupled to silk matrices as described above for GRGDS (SEQ ID NO: 7).